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    /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
    /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
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    /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
    /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
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US-09-956-604D-82056
US-10-367-832A-7968
US-10-367-832A-52967
US-10-367-832A-47439
US-10-367-832A-47439
US-10-367-832A-35241
US-09-956-604D-71887
US-09-954-429-843
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PCT-US03-16467-23
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US-10-367-832A-37574
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   50785, A
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105387,
7968, Ap
110190, A
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47439, A
11887, A
71887, A
71887, A
843, App
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ULT 2 09-954-429-548 equence 5485, ENERAL INFORMA APPLICANT: Mit TITLE OF INVEN FILE REFERENCE CURRENT APPLIC CURRENT FILING D PRIOR APPLICAT PRIOR FILING D NUMBER OF SEQ SOFTWARE: Micr EQ ID NO 5485 LENGTH: 25 TYPE: DNA ORGANISM: Rat OP-954-429-548	Query Match Best Local Matches 1	ULT 1 09-956- equence ENERAL APPLICA TITLE OF FILE RE CURRENT CURRENT CURRENT CURRENT PRIOR A PPIOR F NUMBER SOFTWAR EQ ID N LENGTH TYPE: ORGANI 09-956-	C C C C C C C C C C C C C C C C C C C
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US-10-318-855-17
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US-09-956-604D-135640
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           Sequence 17, Application US/10318855
GENERAL INFORMATION:
APPLICANT: Vincent Ling
APPLICANT: Kyriaki Dunussi-Joannopoulos
TITLE OF INVENTION: NOVEL GL50 MOLECULES AND USES THEREFOR
FILE REFERENCE: GNN-007
CURRENT APPLICATION NUMBER: US/10/318,855
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LENGTH: 25
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TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia Coli
FILE REFERENCE: 3117.1
CURRENT APPLICATION NUMBER: US/09/956,604D
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,049
PRIOR FILING DATE: 2000-09-19
  CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/956,604D
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,049
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOFTWARE: Microarray Probe Sequence Listing Generator
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TITLE OF INVENTION: Methods of Genetic Analysis of
FILE REFERENCE: 3117.1
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ORGANISM: E.
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LENGTH: 25
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US-09-956-604D-105387; Sequence 105387, Application US/09956604D; GENERAL INFORMATION:
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US-09-956-604D-
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SEQ ID NO 105
                                     Query Match
Best Local
                          Matches
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Best Local
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SOFTWARE: FG.
SEQ ID NO 17
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/956,604D CURRENT FILING DATE: 2001-09-19 PRIOR APPLICATION NUMBER: 60/234,049 PRIOR FILING DATE: 2000-09-19 NUMBER OF SEQ ID NOS: 141629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 3117.1

CURRENT APPLICATION NUMBER: US/09/956,604D

CURRENT FILING DATE: 2001-09-19

PRIOR APPLICATION NUMBER: 60/234,049

PRIOR FILING DATE: 2000-09-19

NUMBER OF SEQ ID NOS: 141629

SOFTWARE: Microarray Probe Sequence Listing
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                                                                                                                                                                                                                                    TITLE
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NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4
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TYPE: DI
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                                                                                                   TYPE: DNA
                                                                                                               LENGTH: 25
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E OF INVENTION. Methods of Genetic Analysis
REFERENCE: 3117.1
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82056, App
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INVENTION: Methods of Genetic Analysis
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Pred. No. 2e+0
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                       Score 13.8; DB 5; Pred. No. 2.9e+03; Mismatches 2;
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Pred. No. 2
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2.9e+03;
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RESULT 10
US-09-954-429-10190
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US-10-367-832A-52967
; Sequence 52967, Application US/10367832A
; GENERAL INFORMATION:
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US-10-367-832A-7968/c
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Best Local S
Matches 16
Sequence 10190, Application US/09954429
GENERAL INFORMATION:
APPLICANT: Mittmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3114.1
CURRENT APPLICATION NUMBER: US/09/954,429
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/233,357
PRIOR FILING DATE: 2000-09-18
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EQ ID NO 52967
LENGTH: 23
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LOCATION: (5157777).
OTHER INFORMATION: C
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US-10-367-832A
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Sequence 47439, Application US/10367832A
GENERAL INFORMATION:
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LENGTH: 16
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VENTION: Methods of Genetic Analysis
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Pred. No. 3.6e+03;
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SEQ ID NO 38748
LENGTH: 23
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SEQ ID NO 35241
LENGTH: 24
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SEQ ID NO 4424
LENGTH: 22
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TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,832A
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
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ORGANISM: Pseudomonas
TYPE: DNA
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OTHER INFORMATION: Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                         Match
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                                                                                                                                                                                                                                                                      20 TCCAGCAACTGCTGC 6
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                                                                                                                                                                                                                                                                                                      3 TCCAGCATCTGCTGC 17
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93.38;
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No 4.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                      negative
                                                                                                                                                                                                                                                                                                                                                                     Length 23;
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         Search
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                                                                                     Matches
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Best Local
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OTHER INFO
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me : 90
                                                                                                            Match
                                                                                                                                            INFOR
                                                                                      14
                                         CTCCAGCACCTGCTG 16
                                                                CTCCAGCATCTGCTG 16
                                                                                    67.0%; imilarity 93.3%; Conservative
                                                                                                                                (3432240)...(3432263)
RMATION: Chromosome - 1
-35241
                                                                                                                                                                           Pseudomonas aeruginosa PA01, complete genome
         August 19,
         2003,
                                                                                      0;
                                                                                    Score 13.4; DB 6; Pred. No. 4.4e+03; D; Mismatches 1
          22:11:41
                                                                                                                                         Strand = positive
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